

KW

PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/889,267

DATE: 07/27/2001
 TIME: 19:01:22

Input Set : A:\seqlist.txt
 Output Set: N:\CRF3\07272001\I889267.raw

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4 <110> APPLICANT: Ruelle, Jean-Louis
6 <120> TITLE OF INVENTION: NEISSERIA MENINGITIDIS ANTIGEN
9 <130> FILE REFERENCE: BM45351
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/889,267
C--> 11 <141> CURRENT FILING DATE: 2001-07-13
11 <150> PRIOR APPLICATION NUMBER: PCT/EP00/00137
12 <151> PRIOR FILING DATE: 2000-01-10
14 <160> NUMBER OF SEQ ID NOS: 6
16 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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19 <211> LENGTH: 2169
20 <212> TYPE: DNA
21 <213> ORGANISM: Neisseria meningitidis
23 <400> SEQUENCE: 1
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25 ctttcgtctt cggttttgc cgcacaaacg gcggatttg aaaccgtcca catcaaagg 120
26 cagcgttcgt acaacgcgtat tgtcaccgag aaaaacggcg attacagctc gtttgcgtc 180
27 accgtcgga caaaaatccc cgcttcttg cgcgaaattc cgcaatccgt cagtatcatc 240
28 accaaccagg aggtcaaaga ccgcaatgtt gatacgttt accagttggc gcgaaaaacg 300
29 cccggcctgc gcgtgttag caacgatgac ggacgctt cggtttacgc gcgcgggtac 360
30 gaatacagcg aataacaat cgacggcctg cccgcgcaga tgcagagtat caacggcacg 420
31 ctgccccatc tgttcgcctt cgaccgcgtg gaagtgtatgc gggggcccgag cggactgttc 480
32 gacagcagcg gcgagatggg cgtatcgta aatctggtagt gcaaacgcggcc gaccaaagg 540
33 ttccaagggtc atgctgcggc agggttccgtt acgcacaaac aatataaagc cgaggcggac 600
34 gtatcgggca gcctcaattc agacggcgcgc gtgcgcggcc gcgtgtatggc gcagaccgtc 660
35 ggcgcgtctc cgcgtccgcg cgagaaaaac aaccggcgcg aaaccttcta cgcggcggcg 720
36 gattgggaca tcaaccccgta tacggttttt ggcgcgggt atctttacca gcaacgcac 780
37 ctcgcgcgtt acaacggctt gccagccgtt gccaataaca aattaccgtc cttgcgcac 840
38 cacgtatttg tcggcgccga ttgaaacaaa tttaaaatga acagccacgca cgtgtttgcc 900
39 gatttgaacaa attactcggtt caacggcgccg tacggcaaaatc tggatgtatgc ctattccgac 960
40 cgcgatgccg actccaacta tgcctttgcc ggcagcaagc tggcatgaa aacccggca 1020
41 ggcgcggccgg gctgcaatac ggctgacgac aaaggctgcg cgggtgggtt gggtaacagaa 1080
42 atcaaacaaa aagccctcgat gtttgcgcgc agctacagca ggccttccg cttggcaat 1140
43 acggccaaacg aattttgtcat cgcgcgcgtt tacaaccgtt tccgcagcac caacgaacaa 1200
44 ggcgcgtacta ctttatatgc acgcggcgcc ctggcttacg acgagttccg cagcataccg 1260
45 cagtttattttt tgattgcca cgcgcgcggaa ggcgtgcgcg gttacagcca taccgtcgct 1320
46 accggaaaacc tcgacgaatt cggcattttac ggcacatcca cttccatcc tgccgacggg 1380
47 ctgtcgcttta tcggcgccgg acgtttggga cactataaaa tcgagttccg cgaaggcaaa 1440
48 accctgcaca aagccagcaa aaccaagttc accggctacg caggcgccgt ttacgacttg 1500
49 aacgacaaca acagcctcta cctgagccgtg tcccagctct acacaccgc aaccaaccc 1560
50 gatgccgacg gcaagctgtt caaaccgcgc caaggcaacc agtttgaagt cggttacaaa 1620
51 ggcagctaca tggacgaccg cctcaatgcc ctagttcgt tctaccgcattt gaaagacaaa 1680
52 aacgcgcggc caccgttggaa cccgaacaac aaaaaaacc gttacgcccattt gttggcaaa 1740
53 cgctgtatgg aaggcgttga gaccgaaatc agcggcgccg ttacaccgaa atggcaaaatc 1800
54 catgcaggtt acagctatct gcacagccaa atcaaaaaccg cctccaattt acgcgacgac 1860
55 ggcacatcttcc tgcgtatgcc caaacacagc gcaaaccgtt ggacgactta ccaagttacg 1920
56 cccgagctga ccatcgccgg cggagtgaac gcgatgagcg gcattacttc atctgcagg 1980

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ENTERED

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57 atgcatgcag gcggtatgc cacgttcgat gcgatggcgg cataccgctt cacgcccagg 2040
 58 ctgaagctgc aaatcaacgc cgacaacatc ttcaaccgcc attactacgc ccgcgtcggc 2100
 59 ggcgcgaaca ccttaacat tcccggttcg gagcgcacct ggacggcaaa cctgcgttac 2160
 60 agttttaa 2169
 62 <210> SEQ ID NO: 2
 63 <211> LENGTH: 722
 64 <212> TYPE: PRT
 65 <213> ORGANISM: Neisseria meningitidis
 67 <400> SEQUENCE: 2
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 69 1 5 10 15
 70 Val Leu Ala Ala Leu Ser Ser Ser Val Phe Ala Ala Gln Thr Ala Asp
 71 20 25 30
 72 Leu Glu Thr Val His Ile Lys Gly Gln Arg Ser Tyr Asn Ala Ile Val
 73 35 40 45
 74 Thr Glu Lys Asn Gly Asp Tyr Ser Ser Phe Ala Val Thr Val Gly Thr
 75 50 55 60
 76 Lys Ile Pro Ala Ser Leu Arg Glu Ile Pro Gln Ser Val Ser Ile Ile
 77 65 70 75 80
 78 Thr Asn Gln Gln Val Lys Asp Arg Asn Val Asp Thr Phe Asp Gln Leu
 79 85 90 95
 80 Ala Arg Lys Thr Pro Gly Leu Arg Val Leu Ser Asn Asp Asp Gly Arg
 81 100 105 110
 82 Ser Ser Val Tyr Ala Arg Gly Tyr Glu Tyr Ser Glu Tyr Asn Ile Asp
 83 115 120 125
 84 Gly Leu Pro Ala Gln Met Gln Ser Ile Asn Gly Thr Leu Pro Asn Leu
 85 130 135 140
 86 Phe Ala Phe Asp Arg Val Glu Val Met Arg Gly Pro Ser Gly Leu Phe
 87 145 150 155 160
 88 Asp Ser Ser Gly Glu Met Gly Gly Ile Val Asn Leu Val Arg Lys Arg
 89 165 170 175
 90 Pro Thr Lys Ala Phe Gln Gly His Ala Ala Ala Gly Phe Gly Thr His
 91 180 185 190
 92 Lys Gln Tyr Lys Ala Glu Ala Asp Val Ser Gly Ser Leu Asn Ser Asp
 93 195 200 205
 94 Gly Ser Val Arg Gly Arg Val Met Ala Gln Thr Val Gly Ala Ser Pro
 95 210 215 220
 96 Arg Pro Ala Glu Lys Asn Asn Arg His Glu Thr Phe Tyr Ala Ala Ala
 97 225 230 235 240
 98 Asp Trp Asp Ile Asn Pro Asp Thr Val Leu Gly Ala Gly Tyr Leu Tyr
 99 245 250 255
 100 Gln Gln Arg His Leu Ala Pro Tyr Asn Gly Leu Pro Ala Asp Ala Asn
 101 260 265 270
 102 Asn Lys Leu Pro Ser Leu Pro Gln His Val Phe Val Gly Ala Asp Trp
 103 275 280 285
 104 Asn Lys Phe Lys Met Asn Ser His Asp Val Phe Ala Asp Leu Lys His
 105 290 295 300
 106 Tyr Phe Gly Asn Gly Gly Tyr Gly Lys Val Gly Met Arg Tyr Ser Asp
 107 305 310 315 320

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108 Arg Asp Ala Asp Ser Asn Tyr Ala Phe Ala Gly Ser Lys Leu Gly Met
 109 325 330 335
 110 Lys Thr Pro Ala Gly Arg Pro Gly Cys Asn Thr Ala Asp Asp Lys Ala
 111 340 345 350
 112 Cys Ala Val Gly Leu Gly Thr Glu Ile Lys Gln Lys Ala Leu Ala Phe
 113 355 360 365
 114 Asp Ala Ser Tyr Ser Arg Pro Phe Arg Leu Gly Asn Thr Ala Asn Glu
 115 370 375 380
 116 Phe Val Ile Gly Ala Asp Tyr Asn Arg Phe Arg Ser Thr Asn Glu Gln
 117 385 390 395 400
 118 Gly Arg Thr Thr Leu Tyr Ala Arg Gly Gly Leu Ala Leu Asn Glu Phe
 119 405 410 415
 120 Arg Ser Ile Pro Gln Val Asp Leu Ile Ala Asn Ala Arg Lys Gly Val
 121 420 425 430
 122 Arg Gly Tyr Ser His Thr Val Ala Thr Glu Asn Leu Asp Glu Phe Gly
 123 435 440 445
 124 Ile Tyr Gly Lys Ser Thr Phe His Pro Ala Asp Gly Leu Ser Leu Ile
 125 450 455 460
 126 Gly Gly Arg Leu Gly His Tyr Lys Ile Glu Ser Gly Glu Gly Lys
 127 465 470 475 480
 128 Thr Leu His Lys Ala Ser Lys Thr Lys Phe Thr Gly Tyr Ala Gly Ala
 129 485 490 495
 130 Val Tyr Asp Leu Asn Asp Asn Asn Ser Leu Tyr Leu Ser Leu Ser Gln
 131 500 505 510
 132 Leu Tyr Thr Pro Gln Thr Asn Leu Asp Ala Asp Gly Lys Leu Leu Lys
 133 515 520 525
 134 Pro Arg Gln Gly Asn Gln Phe Glu Val Gly Tyr Lys Gly Ser Tyr Met
 135 530 535 540
 136 Asp Asp Arg Leu Asn Ala Arg Val Ser Phe Tyr Arg Met Lys Asp Lys
 137 545 550 555 560
 138 Asn Ala Ala Ala Pro Leu Asn Pro Asn Asn Lys Lys Thr Arg Tyr Ala
 139 565 570 575
 140 Ala Leu Gly Lys Arg Val Met Glu Gly Val Glu Thr Glu Ile Ser Gly
 141 580 585 590
 142 Ala Val Thr Pro Lys Trp Gln Ile His Ala Gly Tyr Ser Tyr Leu His
 143 595 600 605
 144 Ser Gln Ile Lys Thr Ala Ser Asn Ser Arg Asp Asp Gly Ile Phe Leu
 145 610 615 620
 146 Leu Met Pro Lys His Ser Ala Asn Leu Trp Thr Thr Tyr Gln Val Thr
 147 625 630 635 640
 148 Pro Glu Leu Thr Ile Gly Gly Val Asn Ala Met Ser Gly Ile Thr
 149 645 650 655
 150 Ser Ser Ala Gly Met His Ala Gly Gly Tyr Ala Thr Phe Asp Ala Met
 151 660 665 670
 152 Ala Ala Tyr Arg Phe Thr Pro Lys Leu Lys Leu Gln Ile Asn Ala Asp
 153 675 680 685
 154 Asn Ile Phe Asn Arg His Tyr Tyr Ala Arg Val Gly Gly Ala Asn Thr
 155 690 695 700
 156 Phe Asn Ile Pro Gly Ser Glu Arg Thr Trp Thr Ala Asn Leu Arg Tyr

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157	705	710	715	720
158	Ser Phe			
161	<210> SEQ ID NO: 3			
162	<211> LENGTH: 2078			
163	<212> TYPE: DNA			
164	<213> ORGANISM: Neisseria meningitidis			
166	<400> SEQUENCE: 3			
167	ccatggttgg aaaccgtcac atcaaaggc agcgttcgta caacgcgatt gtcaccgaga	60		
168	aaaacggcga ttacagctcg tttgccgtca ccgtcggcac aaaaatcccc gcttcttgc	120		
169	gcgaaattcc gcaatccgtc agtatcatca ccaaccagca ggtcaaagac cgcaatgttg	180		
170	atacggttgc ccagttggcg cgcaaaacgc ccggcctgcg cgtgttgagc aacgatgacg	240		
171	gacgctcttc ggtttacgcg cgcgggtacg aatacagcga atacaacatc gacggcctgc	300		
172	ccgcgcagat gcagagtatc aacggcacgc tgcccaatct gttcgccttc gaccgcgtgg	360		
173	aagtgtatgcg cgggcccggc ggactgttcg acagcagcgg cgagatggc ggtatcgtga	420		
174	atctggtgcc caaacggcccg accaaagcgt tccaaggcgtca tgctcgccgca ggggtcggta	480		
175	cgcacaaaaca atataaagcc gaggcggacg tatcgggcag cctcaattca gacggcagcg	540		
176	tgcgcggccg cgtatggcg cagaccgtcg gcgcgtctcc gcgtccccc gagaaaaaaca	600		
177	accggcacga aaccttctac gcggcggcgg attgggacat caaccccgat acggtttgg	660		
178	gcgccggcta tcttaccag caacgcccacc tcgcgcgtca caacggcttg ccagccatg	720		
179	ccaataacaa attaccgtcc ctgcccac acgtatttgt cggcgcggat tggaaacaaat	780		
180	ttaaaatgaa cagccacgac gtgttgcg atttggaaaca ttacttcggc aacggcggct	840		
181	acggcaaagt cggatgtcgcc tattccgacc gcgcgtccga ctccaaactat gccttgcg	900		
182	gcagcaagct gggcatgaaa accccggcag gccgcggccgg ctgcaatacg gctgacgaca	960		
183	aaggcctgcgc ggtgggtttg ggtacagaaa tcaaacaaaa agccctcgcg tttgacgca	1020		
184	gctacagcag gccttccgc ttgggcaata cggccaacga atttgcatac ggcgcggatt	1080		
185	acaaccgctt ccgcagcacc aacgaacaag gccgtactac tttatatgca cgcggcggcc	1140		
186	tggctttaaa cgagtccgc agcataccgc aggttgattt gattgccaac gcgcgcaaag	1200		
187	gcgtgcgcgg ttacagccat accgtcgta cggaaaacct cgacgaattc ggcatttacg	1260		
188	gcaaatccac cttccatcct gccgacggc tgtcgttat cggcggcggc cggttggac	1320		
189	actataaaat cgagtccggc gaaggcaaaa ccctgcacaa agccagcaaa accaagttca	1380		
190	ccggctacgc aggccgggt tacgacttga acgacaacaa cagcctctac ctgagcctgt	1440		
191	cccgactcta cacaccgcaa accaacctcg atgcccacgg caagctgctc aaaccgcgc	1500		
192	aaggcaacca gtttgaagtc gtttacaaaag gcagctacat ggacgaccgc ctcaatgccc	1560		
193	gagtttcgtt ctaccgcattaa aagacaaaaa acgcccgc accgttgaac cggaaacaa	1620		
194	aaaaaaacccg ttacgcccga ttgggcaaaac gcgtatggc aggcgtttag accgaaatca	1680		
195	gccccgcggc tacaccgaaa tggcaaatcc atgcaggtt cagctatctg cacagccaaa	1740		
196	tcaaaaacccgc ctccaaattca cgcgacgacg gcatcttctt gctgatgccc aaacacagcg	1800		
197	caaacctgtg gacgacttac caagttacgc ccgagctgac catccgcggc ggagtgaacg	1860		
198	cgatgagcgg cattacttca tctgcaggga tgcgtgcagg cggttatgcc acgttcgtat	1920		
199	cgatggcggc ataccgttc acgcccacgc tgaagctgca aatcaacgac gacaacatct	1980		
200	tcaaccgcac ttactacgcg cgcgtcggc ggcgaacac cttaacatt cccgggttcgg	2040		
201	agcgcagcct gacggcaaac ctgcgttaca gttttaa	2078		
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204	<211> LENGTH: 691			
205	<212> TYPE: PRT			
206	<213> ORGANISM: Neisseria meningitidis			
208	<400> SEQUENCE: 4			
209	Met Val Gly Asn Arg His Ile Lys Gly Gln Arg Ser Tyr Asn Ala Ile			
210	1	5	10	15

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211 Val Thr Glu Lys Asn Gly Asp Tyr Ser Ser Phe Ala Val Thr Val Gly
212      20          25          30
213 Thr Lys Ile Pro Ala Ser Leu Arg Glu Ile Pro Gln Ser Val Ser Ile
214      35          40          45
215 Ile Thr Asn Gln Gln Val Lys Asp Arg Asn Val Asp Thr Phe Asp Gln
216      50          55          60
217 Leu Ala Arg Lys Thr Pro Gly Leu Arg Val Leu Ser Asn Asp Asp Gly
218      65          70          75          80
219 Arg Ser Ser Val Tyr Ala Arg Gly Tyr Glu Tyr Ser Glu Tyr Asn Ile
220      85          90          95
221 Asp Gly Leu Pro Ala Gln Met Gln Ser Ile Asn Gly Thr Leu Pro Asn
222      100         105         110
223 Leu Phe Ala Phe Asp Arg Val Glu Val Met Arg Gly Pro Ser Gly Leu
224      115         120         125
225 Phe Asp Ser Ser Gly Glu Met Gly Gly Ile Val Asn Leu Val Arg Lys
226      130         135         140
227 Arg Pro Thr Lys Ala Phe Gln Gly His Ala Ala Ala Gly Phe Gly Thr
228      145         150         155         160
229 His Lys Gln Tyr Lys Ala Glu Ala Asp Val Ser Gly Ser Leu Asn Ser
230      165         170         175
231 Asp Gly Ser Val Arg Gly Arg Val Met Ala Gln Thr Val Gly Ala Ser
232      180         185         190
233 Pro Arg Pro Ala Glu Lys Asn Asn Arg His Glu Thr Phe Tyr Ala Ala
234      195         200         205
235 Ala Asp Trp Asp Ile Asn Pro Asp Thr Val Leu Gly Ala Gly Tyr Leu
236      210         215         220
237 Tyr Gln Gln Arg His Leu Ala Pro Tyr Asn Gly Leu Pro Ala Asp Ala
238      225         230         235         240
239 Asn Asn Lys Leu Pro Ser Leu Pro Gln His Val Phe Val Gly Ala Asp
240      245         250         255
241 Trp Asn Lys Phe Lys Met Asn Ser His Asp Val Phe Ala Asp Leu Lys
242      260         265         270
243 His Tyr Phe Gly Asn Gly Gly Tyr Gly Lys Val Gly Met Arg Tyr Ser
244      275         280         285
245 Asp Arg Asp Ala Asp Ser Asn Tyr Ala Phe Ala Gly Ser Lys Leu Gly
246      290         295         300
247 Met Lys Thr Pro Ala Gly Arg Pro Gly Cys Asn Thr Ala Asp Asp Lys
248      305         310         315         320
249 Ala Cys Ala Val Gly Leu Gly Thr Glu Ile Lys Gln Lys Ala Leu Ala
250      325         330         335
251 Phe Asp Ala Ser Tyr Ser Arg Pro Phe Arg Leu Gly Asn Thr Ala Asn
252      340         345         350
253 Glu Phe Val Ile Gly Ala Asp Tyr Asn Arg Phe Arg Ser Thr Asn Glu
254      355         360         365
255 Gln Gly Arg Thr Thr Leu Tyr Ala Arg Gly Gly Leu Ala Leu Asn Glu
256      370         375         380
257 Phe Arg Ser Ile Pro Gln Val Asp Leu Ile Ala Asn Ala Arg Lys Gly
258      385         390         395         400
259 Val Arg Gly Tyr Ser His Thr Val Ala Thr Glu Asn Leu Asp Glu Phe

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VERIFICATION SUMMARY

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DATE: 07/27/2001

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Input Set : A:\seqlist.txt

Output Set: N:\CRF3\07272001\I889267.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date